

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



Applicants : Michael Graham Gore et al.
Application No. : 09/808,212
Filed : March 13, 2001
For : IMMUNOGLOBULIN BINDING PROTEIN

Art Unit : 1645
Docket No. : 100084.414US
Date : November 7, 2001

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Commissioner for Patents
Washington, D.C. 20231

DECLARATION

Sir:

I, Monica Steinborn, in accordance with 37 C.F.R. § 1.821(f) do hereby declare that, to the best of my knowledge, the content of the paper entitled "Sequence Listing" and the computer readable copy contained within the floppy disk are the same.

I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated this 7th day of November, 2001.



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#5

1

SEQUENCE LISTING

<110> Gore, Michael Graham
Beckingham, Jennifer Ann
Roberts, Sian Eleri

<120> IMMUNOGLOBULIN BINDING PROTEIN

<130> 100084.414US

<140> 09/808,212

<141> 2001-03-13

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cca aaa gaa gaa gtt aca atc aaa gtt aac tta atc ttt gca gat gga 96
Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
20 25 30

aag ata caa aca gca gaa ttc aaa gga aca ttt gaa gaa gca aca gca 144
Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
35 40 45

gaa gct tac aga tat gca gac tta tta gca aaa gta aat ggc gaa tat 192
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50 55 60

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Gly Lys

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 20 25 30
 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45
 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
 50 55 60
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
 65 70 75 80
 Gly Lys

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 1 5 10 15
 aca atc aaa gct aac cta atc ttt gca aat gga agc aca caa act gca 96
 Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala
 20 25 30
 gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg tat 144
 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
 35 40 45
 gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt gca 192
 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
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Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
          35           40           45
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aac tta atc tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga 96
Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
          20           25           30

aca ttt gaa gaa gca aca gca gaa gca tac aga tat gca gat gca tta 144
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
          35           40           45

aag aag gac aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat 192
Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
          50           55           60

act tta aat att aaa ttt gct gga 216
Thr Leu Asn Ile Lys Phe Ala Gly
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20           25           30
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
35           40           45
Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
50           55           60
Thr Leu Asn Ile Lys Phe Ala Gly
65           70

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Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
1           5           10           15

aac tta atc tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga 96
Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
20           25           30

aca ttt gaa gaa gca aca gca gaa gca tac aga tat gct gac tta tta 144
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
35           40           45

gca aaa gaa aat ggt aaa tat aca gta gac gtt gca gat aaa ggt tat 192
Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
50           55           60

act tta aat att aaa ttt gct gga 216
Thr Leu Asn Ile Lys Phe Ala Gly
65           70

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1           5           10           15
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20           25           30
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
35           40           45

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Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 50 55 60
 Thr Leu Asn Ile Lys Phe Ala Gly
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 <222> (1)...(216)

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 1 5 10 15
 aac tta atc tat gca gat gga aaa act caa aca gca gag ttc aaa gga 96
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 20 25 30
 aca ttt gca gaa gca aca gca gaa gca tac aga tac gct gac tta tta 144
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45
 gca aaa gaa aat ggt aaa tat aca gca gac tta gaa gat ggt gga tac 192
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 50 55 60
 act att aat att aga ttt gca ggt 216
 Thr Ile Asn Ile Arg Phe Ala Gly
 65 70

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 20 25 30
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 50 55 60
 Thr Ile Asn Ile Arg Phe Ala Gly
 65 70

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 1 5 10 15
 atc ttt gca gat gga agc aca caa aat gca gaa ttc aaa gga aca ttc 96
 Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe
 20 25 30
 gca aaa gca gta tca gat gct tac gct tac gca gat gct tta aag aaa 144
 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys
 35 40 45
 gac aac gga gaa tat act gta gac gtt gca gat aaa ggc tta act tta 192
 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu
 50 55 60
 aat att aaa ttc gct ggt aaa 213
 Asn Ile Lys Phe Ala Gly Lys
 65 70

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 <212> PRT
 <213> Peptostreptococcus sp.

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 20 25 30
 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys
 35 40 45
 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu
 50 55 60
 Asn Ile Lys Phe Ala Gly Lys
 65 70

<210> 13
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 <213> Peptostreptococcus sp.

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<221> CDS

<222> (1)...(213)

<400> 13

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  1             5             10             15

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tta atc ttt gca gat gga aag aca caa aca gca gaa ttc aaa gga aca 96
Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr
          20             25             30

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ttt gaa gaa gca aca gca aaa gct tat gct tat gca gac tta tta gca 144
Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala
      35             40             45

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aaa gaa aat ggc gaa tat aca gca gac tta gaa gat ggt gga aac aca 192
Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr
      50             55             60

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Ile Asn Ile Lys Phe Ala Gly
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Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr
      20             25             30

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Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala
      35             40             45

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Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr
      50             55             60

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Ile Asn Ile Lys Phe Ala Gly
  65             70

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<221> CDS

<222> (1)...(222)

<400> 15

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aaa gaa aca cca gaa aca cca gaa gaa cca aaa gaa gaa gtt aca atc 48
Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile
1           5           10           15

```

```

aaa gtt aac tta atc ttt gca gat gga aag ata caa aca gca gaa ttc 96
Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe
           20           25           30

```

```

aaa gga aca ttt gaa gaa gca aca gca aaa gct tat gct tat gca aac 144
Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn
           35           40           45

```

```

tta tta gca aaa gaa aat ggc gaa tat aca gca gac tta gaa gat ggt 192
Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
           50           55           60

```

```

gga aac aca atc aac att aaa ttt gct gga 222
Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly
65           70

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<212> PRT

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           20           25           30
Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn
           35           40           45
Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
           50           55           60
Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly
65           70

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<210> 17

<211> 225

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<213> Peptostreptococcus sp.

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<221> CDS

<222> (1)...(225)

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1           5           10           15

```

aaa gtt aac tta atc ttt gca gat gga aaa aca caa aca gca gaa ttc 96
 Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe
 20 25 30

aaa gga aca ttt gaa gaa gca aca gca gaa gct tac aga tat gca gac 144
 Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp
 35 40 45

tta tta gca aaa gta aat ggt gaa tac aca gca gac tta gaa gat ggc 192
 Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
 50 55 60

gga tac act atc aac atc aaa ttt gct gga aaa 225
 Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys
 65 70 75

<210> 18
 <211> 75
 <212> PRT
 <213> Peptostreptococcus sp.

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 20 25 30
 Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp
 35 40 45
 Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly
 50 55 60
 Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys
 65 70 75

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cca aaa gaa gaa gtt aca atc aaa gtt aac tta atc ttt gca gat gga 96
 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
 20 25 30

aag ata caa aca gca gaa cat aaa gga aca ttt gaa gaa gca aca gca 144
 Lys Ile Gln Thr Ala Glu His Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45

gaa gct tac aga tat gca gac tta tta gca aaa gta aat ggc gaa tat 192
 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
 50 55 60

aca gca gac tta gaa gat ggt gga aac cat atg aac att aaa ttt gct 240
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gga aaa taa 249
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<210> .20

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 1 5 10 15

cca aaa gaa gaa gtt aca atc aaa gtt aac tta atc ttt gca gat gga 96
 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
 20 25 30

aag ata caa aca gca gaa ttc aaa gga aca ttt gaa gaa gca aca gca 144
 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45

gaa gct tac aga aac gca gac tta tta gca aaa gta aat ggc gaa tat 192
 Glu Ala Tyr Arg Asn Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
 50 55 60

aca gca gac tta gaa gat ggt gga aac cat atg aac att aaa ttt gct 240
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
 65 70 75 80

gga aaa taa 249
 Gly Lys

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 1 5 10 15
 cca aaa gaa gaa gtt aca atc aaa gtt aac tta atc ttt gca gat gga 96
 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
 20 25 30
 aag ata caa aca gca gaa ttc aaa gga aca ttt gaa gaa gca aca gca 144
 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
 35 40 45
 gaa gct tac aga tat gca gac tta gac gca aaa gta aat ggc gaa tgg 192
 Glu Ala Tyr Arg Tyr Ala Asp Leu Asp Ala Lys Val Asn Gly Glu Trp
 50 55 60
 aca gca gac tta gaa gat ggt gga aac cat atg aac att aaa ttt gct 240
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
 65 70 75 80
 gga aaa taa 249
 Gly Lys

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 <222> (1)...(246)

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 1 5 10 15

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cca aaa gaa gaa gtt aca atc aaa gtt aac tta atc ttt gca gat gga 96
Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
      20                      25                      30

aag ata caa aca gca gaa ttc aaa gga aca ttt gaa gaa gca aca gca 144
Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
      35                      40                      45

gaa gct tac aga tat gca gac tta cat gca aaa gta aat ggc gaa tat 192
Glu Ala Tyr Arg Tyr Ala Asp Leu His Ala Lys Val Asn Gly Glu Tyr
      50                      55                      60

aca gca gac tta gaa gat ggt gga aac cat atg aac att aaa ttt gct 240
Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
      65                      70                      75                      80

gga aaa taa 249
Gly Lys

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<212> DNA
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<220>
<223> Oligonucleotide used to generate mutations

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<210> 24
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<212> DNA
<213> Artificial Sequence

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<220>
<223> Oligonucleotide used to generate mutations

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<400> 24
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<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

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<220>
<223> Oligonucleotide used to generate mutations

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<213> Artificial Sequence

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<223> Oligonucleotide used to generate mutations

<400> 26
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<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide used to generate mutations

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide used to generate mutations

<400> 28
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<210> 29
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide used to generate mutations

<400> 29
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<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide used to generate mutations

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<213> Artificial Sequence

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<223> primer for the A2N mutation

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33

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<220>
<223> primer for the F39W mutation

<400> 32
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35